

```

      -5              1              5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
  10              15              20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
  25              30              35              40
Ala Phe Ile Asn Xaa Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
      45              50              55
Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu
      60              65              70

```

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLLASGTTLFCTS/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

```

Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly
  -80              -75              -70
Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Xaa Phe
  -65              -60              -55              -50
Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His
      -45              -40              -35
Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro
      -30              -25              -20
Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr
      -15              -10              -5
Ser Phe Tyr Tyr Gln Ala Gln
  1              5

```

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.5
 seq LLTLLLPPPPPLYT/RH
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
-20 -15 -10

Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
-5 1 5 10

Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
15 20 25

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -20..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.5
 seq ILFLLPSICSSNS/TG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys
-20 -15 -10 -5

Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val

1 5 10
Val Thr Thr Thr Xaa Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu
15 20 25
Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Xaa Lys Gly Thr
30 35 40
Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Xaa Phe
45 50 55 60

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
-15 -10 -5
Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
1 5 10
Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
15 20 25
Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
30 35 40 45
Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu
50 55 60
Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
65 70 75
Lys Gln Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu
80 85 90
Val Val Trp Val Asp
95

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

```

Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala Leu Ala Ala
-15          -10          -5          1
Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp Pro Trp Lys
      5          10          15
Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Gln Gln Val Ser Asn
      20          25          30
Leu Ile His Tyr Leu Gly Leu Ser His His Leu Leu Ala Leu Asn Phe
      35          40          45
Ile Ile Val Ser Phe Gly Lys Lys Ser Ala Trp Ser Ser Ala Gln Val
      50          55          60          65
Lys Val Thr Asp Thr Asp Phe Asp Gly Val Glu Val Arg Val Phe Glu
      70          75          80
Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys Arg Ser Val Val Tyr Ile
      85          90          95
His Gly Xaa Gly Trp
      100

```

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Met
40 45

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -69..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq ILLIVLFLDAVRE/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Thr Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile
-65 -60 -55
Gly Leu Ile Leu Ile Phe Cys Leu Pro Phe Ile Pro Pro Gln Arg Trp
-50 -45 -40
Gln Lys Ile Phe Ser Phe Asn Val Trp Gly Lys Ile Ala Thr Phe Trp

-35 -30 -25
 Asn Lys Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu
 -20 -15 -10
 Asp Ala Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu
 -5 1 5 10
 Lys Ser Ser Thr Ser Arg Pro Arg
 15

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq FLDFCVYIPLSWG/FC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
 -85 -80 -75 -70
 Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
 -65 -60 -55
 Glu Val Ser Gly Gly Pro Gly Gly Arg Arg Pro Phe Arg Pro Leu Ala
 -50 -45 -40
 Thr Glu Thr Phe Ser Leu Ala Val Gly Thr Phe Cys Ser Arg Glu Pro
 -35 -30 -25
 Val Gln Ser Asn Asn Leu His Leu Phe Leu Asp Phe Cys Val Tyr Ile
 -20 -15 -10
 Pro Leu Ser Trp Gly Phe Cys Pro Leu Gln Pro Ile Leu Ala
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq AILGSTWVALTTG/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
 -20 -15 -10
Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
 -5 1 5
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
 10 15 20
Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe
 25 30 35 40
His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu
 45 50 55
Ala Arg Ala Asp Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa
 60 65 70
Pro Phe Leu Cys Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro
 75 80 85
Gly

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.2
seq FLVSNMLLAAYG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
-20 -15 -10
Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
-5 1 5 10
Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
15 20 25
Trp Leu Asp Ala Gln Ser Gly
30

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq SVLVLLLLLAVLYE/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe His
-40 -35 -30
Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu Val
-25 -20 -15 -10
Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys Ala
-5 1 5
Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser Gln
10 15 20
Gln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser Phe
25 30 35
Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly Gln
40 45 50 55

Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met Leu
 60 65 70
 Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val
 75 80 85

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VVXXSVLXTTCXS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala
 -75 -70 -65 -60
 Gln Ala Gln Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg
 -55 -50 -45
 Leu Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile
 -40 -35 -30
 Asp Ala Gly Xaa Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val
 -25 -20 -15
 Xaa Xaa Ser Val Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq LLAALMLVAMLQL/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr Gln Leu Leu Leu
-25 -20 -15

Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu Tyr Leu Ser Leu
-10 -5 1 5

Leu Ser Gly Leu His Gly Pro
10

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val
-15 -10 -5

Cys Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro
1 5 10

Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr Ala Pro Met
15 20 25

Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro Glu
30 35 40

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```
Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe
    -20                      -15                      -10

Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
    -5                      1                      5                      10

Leu Gln Cys Ser Val Gly Ile
                15
```

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LMAFLLSFYLIPT/NE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```
Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys
    -50                      -45                      -40

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
    -35                      -30                      -25
```

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
-20 -15 -10 -5

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
1 5 10

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
15 20 25

Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile
30 35 40

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LEMLTAFASHIRA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr Ala Phe Ala
-20 -15 -10

Ser His Ile Arg Ala Arg Asp Ala Ser Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Val His Lys Pro Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile
 -20 -15 -10
His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr
 -5 1 5
Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
 10 15 20
Thr Thr
 25

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
 -25 -20 -15
Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
 -10 -5 1
Tyr Trp Pro Thr
 5

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

```
Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val
-20                      -15                      -10

Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr
-5                      1                      5                      10

Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile
15                      20                      25

Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu
30                      35                      40

Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln
45                      50                      55

Met Arg Asn Ser Gln Ala His Arg
60                      65
```

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -87..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq SNILLASVGSVLG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

```
Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
```

-85 -80 -75
 Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
 -70 -65 -60
 Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile
 -55 -50 -45 -40
 Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
 -35 -30 -25
 Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
 -20 -15 -10
 Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Xaa
 -5 1 5
 Ser Leu Pro Ala Glu Pro Xaa Xaa Xaa Glu Asp Glu Ala Arg Glu Asn
 10 15 20 25
 Val Pro Pro

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq VTIILLSCXFWA/VK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Val Thr Ile Ile Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys
 -10 -5 1
 Asn Val Thr Xaa Arg Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lung

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -87..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Xaa Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
-85 -80 -75
Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
-70 -65 -60
Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile
-55 -50 -45 -40
Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
-35 -30 -25
Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
-20 -15 -10
Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser
-5 1 5
Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn
10 15 20 25
Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His
30 35 40
Glu Arg

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -89..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq DLSLLSLPPGTSP/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
               -85                      -80                      -75

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Xaa Xaa Gly Arg Asn
               -70                      -65                      -60

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu
               -55                      -50                      -45

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
               -40                      -35                      -30

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu
               -25                      -20                      -15                      -10

Leu Ser Leu Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu
               -5                      1                      5

Ala Pro Ile Pro Pro Thr Xaa Leu Ala Xaa Ala Xaa Cys Trp Ala Pro
               10                      15                      20

Ser Val Arg Trp Thr Cys
               25
  
```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LLLPRVLLTMASG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

```

Met Pro Xaa Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
               -20                      -15                      -10

Val Leu Leu Thr Met Ala Ser Gly Ser Leu Arg Xaa Ser Xaa Arg Arg
               -5                      1                      5
  
```

Pro Arg Ile Pro Xaa Leu Ala Thr Phe Arg Xaa Arg Ser Leu
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
 -35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
 -15 -10 -5

Cys Arg Cys Ala Gln Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp
 1 5 10

Gly Ser Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val
 15 20 25

Glu Gly Arg Val Val Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu
 30 35 40 45

Arg Lys Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu
 50 55 60

Xaa Thr Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn
 65 70 75

Gly Cys Thr Lys Ile Thr Xaa Ser Thr Cys
 80 85

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

```
Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
-35                -30                -25                -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
                -15                -10                -5

Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp
                1                5                10

Gly Ser Asn Trp Gln Gly
15
```

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -112..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq SSCILPWLSKTNS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```
Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu Pro Ser Asp Pro Glu
-110                -105                -100

Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala Arg Ser Leu Phe
-95                -90                -85
```

Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val Asp Trp Asp His
 -80 -75 -70 -65
 His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu Asn Leu Pro Arg
 -60 -55 -50
 Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys Pro Val Cys Leu
 -45 -40 -35
 Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met Pro Cys His His
 -30 -25 -20
 Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser Lys Thr Asn Ser
 -15 -10 -5
 Cys Pro Leu Cys Arg Tyr Glu Leu Pro Thr Asp Asp Asp Thr Tyr Glu
 1 5 10 15
 Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln Gln His Arg Pro
 20 25 30

Xaa

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
 -15 -10 -5 1
 Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
 5 10 15
 Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln Pro Ser Pro
 20 25 30
 Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu Gln Pro Arg
 35 40 45
 Pro Gly

50

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LRRLLGCLTLTLS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Leu Gly Ile Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu
-70 -65 -60

Gly Leu Glu Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly
-55 -50 -45

Ser Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn
-40 -35 -30

Glu Ala Arg Gly Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu
-25 -20 -15 -10

Leu Gly Cys Leu Thr Leu Thr Leu Ser Gly Arg Ile
-5 1

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq ALKLASWTSMALA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
-15 -10 -5
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
1 5 10 15
Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
20 25 30
Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
35 40 45
Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
50 55 60
Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
65 70

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq AALPAWLSLQSRA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser Arg Ala
-15 -10 -5
Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr Pro Val
1 5 10 15
Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro
20 25 30
Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Asp Gln
35 40 45

```

Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro Ser Ala
 50                      55                      60

Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro
 65                      70                      75                      80

Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn Phe Leu
                      85                      90                      95

His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu Lys Asp
 100                      105                      110

Phe Cys Thr Glu
 115

```

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CMLTLXXLSFILA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

```

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65                      -60                      -55                      -50

Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
-45                      -40                      -35

Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
-30                      -25                      -20

Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
-15                      -10                      -5

Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
 1                      5                      10                      15

Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
 20                      25                      30

Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
 35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
-45 -40 -35

Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val Ala Ala Thr
-30 -25 -20

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
-15 -10 -5

Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
1 5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LXGFLFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val Ile Val Leu
 -15 -10 -5

Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg Trp Gly Cys
 1 5 10

Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr Pro Asp Asn
 15 20 25 30

Phe Cys Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq VVFMTVAASGASS/FA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu
 -25 -20 -15

Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe Ala Val
 -10 -5 1

Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
 5 10 15

Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr
 20 25 30 35

Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg
 40 45 50

Val Thr

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Glu Leu Ala His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln
-15 -10 -5 1
Ile Thr Glu Ala Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe
5 10 15
Leu Asp Lys Val Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys
20 25 30
Gln Lys Lys Leu Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro
35 40 45
Gly Pro Thr Gly
50

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu
-25 -20 -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp
 -10 -5 1
 Leu Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser
 5 10 15 20
 Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys
 25 30 35
 Arg Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser
 40 45 50
 Gly Gln Arg Val Phe Val Val Lys Arg Gly
 55 60

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LVGVLFVSVTTG/PW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
 -30 -25 -20
 Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
 -15 -10 -5 1
 Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
 5 10 15
 Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 20 25 30
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 35 40 45
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa Ser Gly Asn
 50 55 60 65
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
 70 75 80

Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa Xaa Val Ser
85 90 95
Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
100 105 110
Phe Gly Phe Val
115

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
5 10 15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

```

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
      -10                      -5                      1
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg Asp Leu Gln Gln
      5                      10                      15
Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser
    20                      25                      30                      35
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile
      40                      45                      50
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro
      55                      60                      65
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
      70                      75                      80
Glu Gln
      85

```

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq MMVLSLGIXLASA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

```

Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
      -65                      -60                      -55
Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
      -50                      -45                      -40
Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
      -35                      -30                      -25
Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
      -20                      -15                      -10

```

Xaa Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
 15 20 25
 Ile Ser Gly Ser Leu Ser Ile
 30

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Gly Val Gly Lys Xaa Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85
 Ala Val Xaa Leu Ile Thr Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys
 90 95 100
 Thr Phe Val Thr Trp Phe Leu
 105 110

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
-25                -20                -15                -10

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
          -5                      1                      5

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
      10                      15                      20

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
      25                      30                      35

Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
      40                      45                      50                      55

Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
          60                      65                      70

Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
          75                      80                      85

Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
          90                      95                      100

Thr Phe Val His Val Val Pro
      105                      110

```

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AIALATVFLFLIGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```
Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
      -55                      -50                      -45

Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
      -40                      -35                      -30

Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
      -25                      -20                      -15                      -10

Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
              -5                      1                      5

Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
      10                      15                      20

Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
      25                      30                      35
```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```
Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
```

```

-15              -10              -5              1
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
          5              10              15
Gln His Pro Thr Xaa Gln
      20

```

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15 -10 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
5 10 15

Gln His Pro Thr Gln Cys Ser Thr His Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -63..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

```

Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
      -65                      -60                      -55

Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
      -50                      -45                      -40

Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
      -35                      -30                      -25

Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
-20                      -15                      -10                      -5

His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
      1                      5                      10

Ala

```

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -94..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VILQLQFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```

Met Phe Gly Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln
      -90                      -85                      -80

Arg Asp Ser Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly
      -75                      -70                      -65

Asp Val Val Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr
      -60                      -55                      -50

Leu Gln Gln Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly
      -45                      -40                      -35

Pro Gly Gln Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser

```

-30 -25 -20 -15
Pro Val Ile Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr
 -10 -5 1
Leu Ser Leu Lys Leu Val His Val Ala Gly Pro Gly Pro Thr
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq LILVGTSKHVAFG/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu
-85 -80 -75
Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly
-70 -65 -60 -55
Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
 -50 -45 -40
Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
 -35 -30 -25
Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser
 -20 -15 -10
Lys His Val Ala Phe Gly Lys Ile Ile
 -5 1

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq WYSTVGLLPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys Asp His Gly Thr
-35                -30                -25                -20

Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly Leu Leu Pro Pro
                -15                -10                -5

Val Arg Ala Met Ser Gln Arg Asn Leu Asn
                1                5

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq ARALAALVPGVTQ/VD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Ala Ala Ala Leu Lys Cys Leu Leu Thr Leu Gly Arg Trp Cys Pro
-35                -30                -25

Gly Leu Gly Val Ala Pro Gln Ala Arg Ala Leu Ala Ala Leu Val Pro
-20                -15                -10                -5

Gly Val Thr Gln Val Asp Asn Lys Ser Gly Phe Leu Gln Lys Arg Pro
                1                5                10

His Arg Gln His Pro Gly Ile Leu Lys Leu Pro His Val Arg Leu Pro
15                20                -                25

```


Gln Ala Leu Ala Asn Gly Ala Gln Leu Leu Leu Leu Gly Ser Ala Gly
 30 35 40

Pro Thr Met Glu Asn Gln Val Gln Thr Leu Thr Ser Tyr Leu Trp Ser
 45 50 55 60

Arg His Leu Pro Val Glu Pro Xaa Glu Leu Gln Arg Arg Ala Xaa His
 65 70 75

Leu Glu Lys Lys Phe Leu Glu Asn Pro Asp Leu Ser Gln Thr Glu Glu
 80 85 90

Lys Leu Arg Gly Ala Gly
 95

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -102..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq TVMSALSVAPSKA/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu Ile Lys Gly Ser
 -100 -95 -90

Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly
 -85 -80 -75

Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val
 -70 -65 -60 -55

Pro Pro Ala Met Xaa Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly
 -50 -45 -40

Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile
 -35 -30 -25

Arg Asp Ser Trp Xaa Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser
 -20 -15 -10

Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr
 -5 1 5 10

Val Lys Ala Leu Gly
15

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Val Asn Glu Leu Gln Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala
-15 -10 -5

Cys Ser Ser Ser Lys Gln Arg Phe
1 5

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FFFSIQPFLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala Phe Phe Phe Ser Ile

-20

-15

-10

Gln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu Lys Ser Pro Ser Pro
 -5 1 5

Val Ala His Pro Thr Asn Ile Ser Val Ser Glu Asn Ala Gln Arg Cys
 10 15 20

Leu Xaa Thr Ser Pro Trp
 25 30

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WVIVLTSWITIFQ/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 -75 -70 -65

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
 -60 -55 -50

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
 -45 -40 -35

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
 -30 -25 -20

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
 -15 -10 -5 1

Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile
 5 10 15

Pro Leu Gly Thr Pro Asp Asn Phe Cys Thr Tyr
 20 25

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
-70 -65 -60 -55

Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
 -50 -45 -40

Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn
 -35 -30 -25

Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe
 -20 -15 -10

Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg
 -5 1 5 10

Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn
 15 20 25

Tyr Leu Tyr

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9

seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
-55                               -50                     -45

Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Asn Pro Ser
-40                               -35                     -30                     -25

Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
                               -20                     -15                     -10

Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly
                               -5                               1                     5

Pro Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro
    10                               15                     20

Phe Val
    25

```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Glu Glu Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys
-25                               -20                     -15

Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
-10                               -5                               1                     5

Ser Val Arg Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser
    10                               15                     20

Lys His Leu Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp
    25                               30                     35

```

Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys
40 45 50

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LXXVVAFVAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Val Arg Arg Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu
-15 -10 -5
Ser Gln Gln Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly
1 5 10 15
Gln Glu Arg Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly
20 25 30
Asp Cys Gln Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp
35 40 45
Gly Ser Asp Val Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys
50 55 60
Thr Lys Glu Ala Gly Asp Gly Pro Leu
65 70

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq PIVRLLLSCPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

```

Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn Leu Cys Ala
  -35                      -30                      -25

Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu Leu Ser Cys
  -20                      -15                      -10

Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln Pro Ser Gly
   -5                      1                      5                      10

Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg Arg Phe Ser
      15                      20                      25

Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr Val Leu Ile
      30                      35                      40

His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys Tyr Leu Ser
      45                      50                      55

Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser Phe Gly Leu
      60                      65                      70                      75

Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly Ser Leu Gln
      80                      85                      90

Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala Ile Pro Phe
      95                      100                     105

Arg Ser Arg Ser Ser
      110

```

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LVILSLKSQTLDA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
-60                -55                -50                -45

Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
-40                -35                -30

Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
-25                -20                -15

Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
-10                -5                1

Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
5                10                15                20

Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Xaa
25                30                35

Asn Met Asn Leu Glu Gly Gly
40

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly Asp Ser Gly
-30                -25                -20

Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn Gln Val Leu
-15                -10                -5

Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His
1                5                10                15

Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr Ile Glu Leu
20                25                30

```


Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr
 35 40 45
 Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa Val His Asp
 50 55 60
 Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp Ser Leu Glu
 65 70 75
 Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val
 80 85 90

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly
 -30 -25 -20
 Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu
 -15 -10 -5 1
 Trp Leu Leu Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile
 5 10 15
 Gly Gln Phe Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg
 20 25 30
 Leu Met Ile Arg Lys Leu Val Ala Glu Asn Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
-25 -20 -15
Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5
Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
10 15 20
Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
25 30 35
Cys Ala Arg
40

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys
-30 -25 -20
Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala

```

-15           -10           -5           1
Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
          5             10             15
Ser Val Leu Lys Leu His His Ser Arg Gly
      20             25

```

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq SLAALTLHGHWG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Asp Tyr Ser Leu Ala Ala Ala Leu Thr Leu His Gly His Trp Gly
-15 -10 -5

Leu Gly Gln Val Val Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -72..-1
```

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LSLXASYIFGISG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
 -70 -65 -60

Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
 -55 -50 -45

Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
 -40 -35 -30 -25

Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
 -20 -15 -10

Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
 -5 1 5

Arg Asn Glu Phe Val Arg Gln Ser
 10 15

```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -76..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
 -75 -70 -65

Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
 -60 -55 -50 -45

Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
 -40 -35 -30

Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Xaa Leu
 -25 -20 -15

```

Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser  
 -10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrrenals

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq SVMGVCLLIPGLA/TA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Trp Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu  
 -20 -15 -10

Leu Ile Pro Gly Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg  
 -5 1 5 10

Gly Lys Glu Lys Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met  
 15 20 25

Glu Arg Asp Arg Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys  
 30 35 40

Gly Pro Gly  
 45

## (2) INFORMATION FOR SEQ ID NO: 489:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: -46..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Glu Phe Lys Leu Glu Ala His Arg Ile Val Ser Ile Ser Leu Gly
-45 -40 -35

Lys Ile Tyr Asn Ser Arg Val Gln Arg Gly Gly Ile Lys Leu His Lys
-30 -25 -20 -15

Asn Leu Leu Val Ser Leu Val Leu Arg Xaa Pro Ala Lys Ser Thr Arg
-10 -5 1

Ala Gly

```

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -97..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq IASGLGLXLDCT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
-95 -90 -85

Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
-80 -75 -70

Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
-65 -60 -55 -50

Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
-45 -40 -35

Leu Glu Val Tyr Pro Xaa Phe Leu Phe Phe Leu Ala Val Gly Gly Val
-30 -25 -20

Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Xaa Leu Asp Cys Trp
-15 -10 -5

```

Thr Ser Ser Leu Cys Leu Trp Leu Leu His Gly Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq RIPS L P G S P V C W A / W P

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala  
-40 -35 -30

Met Ser Ser Trp Ala Arg Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro  
-25 -20 -15

Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq R L L L R R F L A S V I S / R K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser  
 -15 -10 -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu  
 1 5 10 15

Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro  
 20 25 30

Ala Arg Thr  
 35

## (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq FLLLLEVSHLLLI/IN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe Leu Leu Leu  
 -25 -20 -15 -10

Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu Gly  
 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 494:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:



(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -77..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg  
-75 -70 -65  
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val  
-60 -55 -50  
Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr  
-45 -40 -35 -30  
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe  
-25 -20 -15  
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys  
-20 -15 -10  
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly  
-5 1 5 10  
Val Tyr Tyr Arg Gly Gly Val  
15

(2) INFORMATION FOR SEQ ID NO: 496:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -25..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.4  
                            seq LVFMVPLVGLIHL/GW
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met  
-25                    -20                    -15                    -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser  
                    -5                            1                            5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp  
            10                            15                            20

Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu  
            25                            30                            35

(2) INFORMATION FOR SEQ ID NO: 497:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Spleen
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -23..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.4  
                            seq VFCLLISIPTPSA/HL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Gly Trp Asp Gly Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile

-20

-15

-10

Ser Ile Pro Thr Pro Ser Ala His Leu  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 498:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -118..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
 seq ILAHLRLGLIPIHA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala Trp Phe Trp  
 -115 -110 -105

Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe Pro Val Thr  
 -100 -95 -90

Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe Glu Xaa Arg  
 -85 -80 -75

Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser Leu Glu Phe  
 -70 -65 -60 -55

Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe Arg Arg Ile  
 -50 -45 -40

Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val Leu Val Tyr  
 -35 -30 -25

Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His Arg Leu Gly  
 -20 -15 -10

Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr Arg Asn Gln  
 -5 1 5 10

Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe Arg Leu Gln  
 15 20 25

Val Arg Cys Thr Arg  
 30

## (2) INFORMATION FOR SEQ ID NO: 499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -77..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq FEARIALLLPLLQA/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
 -75 -70 -65

Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
 -60 -55 -50

Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
 -45 -40 -35 -30

Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
 -25 -20 -15

Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
 -10 -5 1

Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
 5 10 15

Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa Xaa Val Pro
 20 25 30 35

His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq VLFFTGWWIIIDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp  
-40 -35 -30  
Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe  
-25 -20 -15  
Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr  
-10 -5 1 5  
Arg

## (2) INFORMATION FOR SEQ ID NO: 501:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -44..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LVFLTFLSIPSFV/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Met Thr Gln Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg  
-40 -35 -30  
Ile Ile Cys Ser Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu  
-25 -20 -15  
Val Phe Leu Thr Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn  
-10 -5 1  
Ile Arg Ala Glu Thr Phe Leu Gln Asn Val  
5 10

## (2) INFORMATION FOR SEQ ID NO: 502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq FLTALLWRGRIPG/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln  
                  -10                  -5                          1

Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys  
          5                          10                          15

Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp  
      20                          25                          30

Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa  
      35                          40                          45                          50

Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser  
          55                          60                          65

Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Xaa  
          70                          75                          80

Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu  
      85                          90                          95

Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys  
      100                          105                          110

Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr  
      115                          120                          125

## (2) INFORMATION FOR SEQ ID NO: 503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

```
Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
-90 -85 -30 -75

Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly
 -70 -65 -60

Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln
 -55 -50 -45

Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
 -40 -35 -30

Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
 -25 -20 -15

Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp
-10 -5 1
```

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

```

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu
 -50 -45 -40
Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val Leu Leu Pro
 -35 -30 -25
Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp Leu Leu Val
 -20 -15 -10
Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
 -5 1 5 10
Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
 15 20 25
Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
 30 35 40
Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys His Arg Xaa
 45 50 55
Leu His His Tyr Tyr Gly Cys
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq CPTCLCAPSXXWG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu Pro
 -10 -5 1
Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys Lys
 5 10 15
Ala Arg Ser
 20

```

## (2) INFORMATION FOR SEQ ID NO: 506:





-15

-10

-5

Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa Leu Gly Phe Gly Gly Phe  
 1 5 10 15  
 Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala Pro Val Arg His Ser Gly  
 20 25 30  
 Asp His Gly Lys Arg Leu Phe Val Ile Arg Pro Ser Arg Phe Tyr Asp  
 35 40 45  
 Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr Ile Ala Leu Thr Gly Ile  
 50 55 60  
 Pro Val Ala Xaa Phe Ile Thr Leu Val Asn Val Phe Ile Gly Gln Ala  
 65 70 75  
 Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val Pro Glu His Trp Glu Tyr  
 80 85 90 95  
 Tyr Lys His Pro Ile Ser Arg Trp Ile Ala Arg Asn Phe Tyr Asp Ser  
 100 105 110  
 Pro Xaa Lys Ile Tyr Glu Arg Thr Met  
 115 120

## (2) INFORMATION FOR SEQ ID NO: 508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LDLLRGLPRVSLA/NL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu  
 -25 -20 -15 -10  
 Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly  
 -5 1 5  
 Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Gly Arg Lys  
 10 15 20  
 Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg

25

30

35

Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys  
 40 45 50 55  
 Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu  
 60 65 70  
 Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro  
 75 80 85  
 Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr  
 90 95 100  
 Ile Ala Pro  
 105

## (2) INFORMATION FOR SEQ ID NO: 509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq GILILWIIRLLFS/KT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala  
 -40 -35 -30  
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile  
 -25 -20 -15 -10  
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu  
 -5 1 5  
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp  
 10 15 20  
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu  
 25 30 35  
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn  
 40 45 50 55

Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu  
                                 60                                65                                70  
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr  
                                 75                                80                                85  
 Gly Val Gly Thr Cys Gly Pro Cys  
                                 90                                95

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq QGVLFICFTCAR/FP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Glu Asp Pro Asn Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro  
                                 -75                                -70                                -65  
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly  
                                 -60                                -55                                -50  
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa  
                                 -45                                -40                                -35  
 Xaa Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln  
                                 -30                                -25                                -20  
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe  
                                 -15                                -10                                -5                                1  
 Pro Ser

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -32..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His  
-30 -25 -20  
Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn  
-15 -10 -5  
Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr  
1 5 10 15  
His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser  
20 25 30  
Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr Ser  
35 40 45  
Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser Gln  
50 55 60  
Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys Tyr  
65 70 75 80  
Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly Xaa  
85 90 95  
Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly  
100 105 110

## (2) INFORMATION FOR SEQ ID NO: 512:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -58..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1  
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala  
-55 -50 -45  
Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr Gly  
-40 -35 -30  
Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His  
-25 -20 -15  
His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys  
-10 -5 1 5  
Ala Tyr Leu Pro Thr Gly Lys Trp  
10

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Ala Thr Leu Thr Phe Ser Leu Arg Lys Pro Leu Gln Arg Ser Leu  
-85 -80 -75  
Ile Arg Pro Ser His Leu Pro Leu Cys Cys Phe Asp Trp Arg Leu Ser  
-70 -65 -60  
His Tyr Tyr Arg Leu Pro Pro Ala Val Arg Leu His Gln Gln Arg Gly  
-55 -50 -45  
Gly Arg Pro Gly Arg Ser Ser Ala Asp His Trp His Ser Gly Val Pro  
-40 -35 -30 -25  
Thr Arg Ile Leu Pro Pro Ala His Arg Leu Leu Cys Ile Gln Arg Leu  
-20 -15 -10

Pro Trp Leu Leu Leu Cys Arg Gly Ile Thr Ser  
                   -5                                  1

## (2) INFORMATION FOR SEQ ID NO: 514:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq PSLAAGLLFGSXA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe  
                   -45                                  -40                                  -35

Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys  
                   -30                                  -25                                  -20

Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Xaa  
                   -15                                  -10                                  -5

Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp  
                   1                                  5                                  10                                  15

Gly Phe Leu Ala Ala Thr Ser Val  
                                   20

## (2) INFORMATION FOR SEQ ID NO: 515:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4  
seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

```

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly
 -15 -10 -5

Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln
 1 5 10

Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
 15 20 25 30

Tyr Tyr Arg Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala
 35 40 45

Gly

```

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -83..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4  
seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

```

Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
 -80 -75 -70

Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
 -65 -60 -55

Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
 -50 -45 -40

Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Val Gln Gly Pro
 -35 -30 -25 -20

His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg Leu Leu Ser Gln
 -15 -10 -5

```



Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe Ser Gln Tyr Cys  
                   1                                  5                                  10  
 Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe Phe Phe  
           15                                  20                                  25

## (2) INFORMATION FOR SEQ ID NO: 517:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq ITSSLFLGRGSA/SN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala Pro  
           -40                                  -35                                  -30  
 Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr Ser  
           -25                                  -20                                  -15  
 Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu Leu  
           -10                                  -5                                  1                                  5  
 Gln Ala Arg Gly Ile  
                   10

## (2) INFORMATION FOR SEQ ID NO: 518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly Thr  
-15 -10 -5  
Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe Leu  
1 5 10  
Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser Asp  
15 20 25 30  
Phe Glu Lys Val Gln Glu Arg  
35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly  
-15 -10 -5  
Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr  
1 5 10  
Leu

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9  
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr  
-10 -5 1  
Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val  
5 10 15  
Glu Xaa Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe  
20 25 30 35  
Asp Asp Leu Pro Ala Arg Phe Gly Tyr  
40

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9  
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala  
-25 -20 -15 -10  
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys  
-5 1 5  
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His  
10 15 20

```

Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
 25 30 35
Xaa Xaa Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
 40 45 50 55
Pro Phe Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
 60 65 70

```

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq YTAVSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

```

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60 -55 -50
Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45 -40 -35 -30
Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
 -25 -20 -15
Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
 -10 -5 1
Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5 10 15
Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn Gly Arg
 20 25 30 35
Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Ala Ile Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser  
-30                                 -25                                 -20                                 -15

Lys Leu Trp Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile  
                              -10                                 -5                                 1

Xaa Ala Glu Pro Pro Gln Leu Asp Ile Ser  
                  5                                 10

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq FVLGSARLGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu Asp Asp Phe Val  
          -25                                 -20                                 -15

Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met Arg Pro Ala Ala  
          -10                                 -5                                 1                                 5

Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu Pro Asn Gln Leu

10

15

20

Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg Val Arg Thr Ala  
25 30 35

Thr

## (2) INFORMATION FOR SEQ ID NO: 525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LVSATAWLEECWW/SE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Lys Leu Val Ser Ala Thr Ala Trp Leu Glu Glu Cys Trp Trp Ser  
-15 -10 -5 1

Glu Leu Ser

## (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LYVPLLAVCCLHS/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu Leu Trp  
                   -30                  -25                  -20

Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys Cys Leu  
                   -15                  -10                  -5

His Ser Val Val Phe Phe  
                   1

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -118..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
                                   seq LMIALTUVGCIFM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg  
                   -115                  -110                  -105

Leu Cys Glu Arg Asp Val Ser Xaa Ser Leu Arg Leu Thr Arg Ser Ser  
                   -100                  -95                  -90

Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro  
                   -85                  -80                  -75

Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr  
                   -70                  -65                  -60                  -55

Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu  
                   -50                  -45                  -40

Xaa Xaa Ile Pro Glu Thr Val Ser Leu Glu Met Leu Xaa Xaa Ala Lys  
                   -35                  -30                  -25

Asn Lys Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val  
                   -20                  -15                  -10

Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg  
                   -5                  1                  5                  10

His Glu Thr Leu Thr Ser Leu Xaa Leu Glu Lys Lys Ala Arg Leu  
                   15                  20                  25

## (2) INFORMATION FOR SEQ ID NO: 528:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -100..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq LASSFLFTMGGLG/FI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn  
-100 -95 -90 -85

Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr  
-80 -75 -70

Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile  
-65 -60 -55

Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp  
-50 -45 -40

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn  
-35 -30 -25

Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met  
-20 -15 -10 -5

Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile  
1 5 10

Pro Lys Leu Asn Arg Phe  
15

## (2) INFORMATION FOR SEQ ID NO: 529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -13..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq MLVLRSGLTALA/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr  
-10 -5 1  
Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val Arg Lys Ala  
5 10 15  
Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile Pro Asn Leu  
20 25 30 35  
Ala Arg Ile Asp Lys Gln Glu Thr Arg  
40

## (2) INFORMATION FOR SEQ ID NO: 530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -36..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq NIESLAWTGGTLG/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Ala Ala Pro Leu Ser Val Glu Val Glu Phe Gly Gly Gly Ala Xaa  
-35 -30 -25  
Ser Cys Leu Thr Val Leu Arg Asn Ile Glu Ser Leu Ala Trp Thr Gly  
-20 -15 -10 -5  
Gly Thr Leu Gly His Pro Glu Pro Ala His Leu Asp Gln Glu Glu Phe  
1 5 10  
Ala Lys Arg Ala Ala Xaa Val Val His Pro Gly Arg Gln Arg Ala Ala

15

20

25

Arg Asn Ser Gly Ala Asp Tyr Arg  
30 35

## (2) INFORMATION FOR SEQ ID NO: 531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq FVGGLPVIFWSWA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Thr His Leu Ile Glu Tyr Asp Arg His Arg Lys Ser Arg Leu Ser  
-65 -60 -55 -50  
Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp His Ser Arg Asn Ala  
-45 -40 -35  
Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro Pro Thr Val Asp Ser  
-30 -25 -20  
Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val Ile Phe Trp Ser Trp  
-15 -10 -5  
Ala Gly Leu Val  
1

## (2) INFORMATION FOR SEQ ID NO: 532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Ala Ala Ala Ala Leu Gly Gln Ile Trp Ala Arg Lys Leu Leu Ser  
-20 -15 -10  
Val Pro Trp Leu Leu Cys Gly Pro Arg Arg Tyr Ala Ser Ser Ser Phe  
-5 1 5 10  
Lys Ala Ala Asp Leu Gln Leu Glu Met Thr Gln Lys Pro His Lys Lys  
15 20 25  
Pro Gly Pro Gly Glu Pro Leu Val Phe Gly Lys Thr Phe Thr Asp His  
30 35 40  
Met Leu Met Val Glu Trp Asn Asp Lys Gly Trp Gly Gln Pro Arg Ile  
45 50 55  
Gln Pro Phe Gln Asn Leu Thr Leu His Pro Ala Ser Ser Ser Leu His  
60 65 70  
Tyr Ser Leu Gln Leu Phe Glu Gly  
75 80

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq CPLLLLVTNNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Ala Val Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro  
-35 -30 -25  
Glu Lys Pro Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Leu Val  
-20 -15 -10

```

Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg
 -5 1 5 10
Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala
 15 20 25
Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala
 30 35 40
Arg Xaa Lys Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val
 45 50 55
Lys Arg Pro
 60

```

## (2) INFORMATION FOR SEQ ID NO: 534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq AVLDCAFYDPHTA/WS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

```

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 -5 1 5 10
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25
Pro Leu Ser Asp Val Leu
 30

```

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -86..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala  
-85 -80 -75  
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe  
-70 -65 -60 -55  
Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp  
-50 -45 -40  
Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val  
-35 -30 -25  
Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp  
-20 -15 -10  
Thr Ala Val Thr Ser Gly Arg Gly  
-5 1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -68..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln Arg Phe Phe Gln

```

 -65 -60 -55
Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln Ala Ala Leu Glu
 -50 -45 -40
Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp Ala Gln Tyr Tyr
 -35 -30 -25
Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn Tyr Cys Val Ala
 -20 -15 -10 -5
Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro Asn Asn Ser Thr
 1 5 10
Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu Lys Asn Tyr Ala
 15 20 25
Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

```

Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly Tyr Ala Gln Glu Asp
-60 -55 -50 -45
Arg Glu Arg Met His Arg Asn Ile Val Ser Leu Ala Gln Asn Leu Leu
 -40 -35 -30
Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp
 -25 -20 -15
Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro
 -10 -5 1
Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu Asn Ala Ala Trp Pro
 5 10 15 20

```

Arg

## (2) INFORMATION FOR SEQ ID NO: 538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq WSPLSTRSGGTHA/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
-30 -25 -20

Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys  
-15 -10 -5 1

Ser Ala Ser Met Arg Gln Pro Trp  
5

## (2) INFORMATION FOR SEQ ID NO: 539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq SILAQVLDQSARA/RL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Glu | Glu | Leu | Glu | Ala | Leu | Arg | Gln | Arg | Leu | Ala | Glu |     |
|     |     |     | -50 |     |     |     |     |     | -45 |     |     |     | -40 |     |     |
| Leu | Gln | Ala | Lys | His | Gly | Asp | Pro | Gly | Asp | Ala | Ala | Gln | Gln | Glu | Ala |
|     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |
| Lys | His | Arg | Glu | Ala | Glu | Met | Arg | Asn | Ser | Ile | Leu | Ala | Gln | Val | Leu |
|     |     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |
| Asp | Gln | Ser | Ala | Arg | Ala | Arg | Leu | Ser | Asn | Leu | Ala | Leu | Val | Lys | Pro |
|     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |
| Glu | Lys | Thr | Lys | Ala | Val | Glu | Asn | Tyr | Leu | Ile | Gln | Met | Ala | Arg | Tyr |
|     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |
| Gly | Gln | Leu | Ser | Glu | Lys | Val | Ser | Glu | Gln | Gly | Leu | Ile | Glu | Ile | Leu |
|     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |
| Lys | Lys | Val | Ser | Gln | Gln | Thr | Glu | Lys | Xaa | Thr | Thr | Val | Arg |     |     |
|     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -63..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
                        seq GLVCAGLADMARPAE
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met	Ser	Ala	Ala	Gly	Ala	Arg	Gly	Leu	Arg	Ala	Thr	Tyr	His	Arg	Leu
			-60					-55					-50		
Leu	Asp	Lys	Val	Glu	Leu	Met	Leu	Pro	Glu	Lys	Leu	Arg	Pro	Leu	Tyr
		-45					-40					-35			
Asn	His	Pro	Ala	Gly	Pro	Arg	Thr	Val	Phe	Phe	Trp	Ala	Pro	Ile	Met
	-30					-25					-20				
Lys	Trp	Gly	Leu	Val	Cys	Ala	Gly	Leu	Ala	Asp	Met	Ala	Arg	Pro	Ala
-15					-10					-5					1
Glu	Lys	Leu	Ser	Thr	Ala	Gln	Ser	Xaa	Val	Leu	Met	Ala	Thr	Gly	Phe
			5					10					15		

Ile Trp Ser Arg Tyr Ser
20

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Ser Asn Tyr Ser Val Ser Leu Val Gly Pro Ala Pro Trp Gly Phe
-85                               -80                               -75

Arg Leu Gln Gly Gly Lys Asp Phe Asn Met Pro Leu Thr Ile Ser Ser
-70                               -65                               -60                               -55

Leu Lys Asp Gly Gly Lys Ala Ala Gln Ala Asn Val Arg Ile Gly Asp
                               -50                               -45                               -40

Val Val Leu Ser Ile Asp Gly Ile Asn Ala Gln Gly Met Thr His Leu
                               -35                               -30                               -25

Glu Ala Gln Asn Lys Ile Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr
                               -20                               -15                               -10

Leu Gln Arg Ala Ser Ala Ala Pro Lys Pro Glu Pro Val Pro Val Gln
                               -5                               1                               5                               10

Lys Pro Thr Val Thr Ser Val Cys Ser Glu Thr Ser Gln Glu Leu Ala
                               15                               20                               25

Glu Gly Gln Arg Arg Gly Ser Gln Gly Asp Ser Lys Gln Gln Asn
                               30                               35                               40

```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEAIG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
-15 -10 -5

Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
1 5 10

Lys Glu Leu Gln Gln
15

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -40..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq ALLCTLHLLHFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ile Ile Pro Leu Leu Glu Ile Leu Ile Ile Ile Val Leu Asn Glu
-40 -35 -30 -25

Val Leu Leu Phe Asp Val Asn Ser Val Tyr Lys Ala Leu Leu Cys Thr
-20 -15 -10

Leu Leu Leu His Phe Gln Asn Ile Arg Arg Phe Leu Ser Ser Gln Ser
-5 1 5

Pro Met Lys Ala Val Ser Leu Leu Xaa Phe His Gln Pro Asp Phe Asp

10

15

20

Tyr Ile
25

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro Pro Ser Ala Thr Pro
   -50                      -45                      -40

Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His Ser Thr Ala Arg Ile
   -35                      -30                      -25

Val Met Pro Leu His Tyr Ser Leu Val Phe Ile Ile Gly Leu Val Gly
   -20                      -15                      -10                      -5

Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn Arg Lys Lys Ile Asn
           1                      5                      10

Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe
           15                      20                      25

Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met Xaa Trp Ala Leu Thr
           30                      35                      40

Gly Glu Ser Glu Met Trp
   45                      50

```

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Pancreas

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser
 -25 -20 -15

Ser Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile
 -10 -5 1

Gln Gln Arg
 5



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47	A3	(11) International Publication Number: WO 99/06548 (43) International Publication Date: 11 February 1999 (11.02.99)
(21) International Application Number: PCT/IB98/01222 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,135 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Régimbeau, 26, Avenue Kléber, F-75116 Paris (FR).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 8 April 1999 (08.04.99)
(54) Title: 5'ESTs FOR NON TISSUE SPECIFIC SECRETED PROTEINS (57) Abstract The sequences of 5'ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5'ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5'ESTs. The 5'ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5'ESTs. The 5'ESTs may also be used to design expression vectors and secretion vectors.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Larvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No

PC1, A B 98/01222

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 98 45437 A (GENETICS INSTITUTE INC. (US); JACOBS K. ET AL.) 15 October 1998 Seq.ID:262 is 97% identical to Seq.ID:38 see page 56 - page 57 see page 63, line 9-17 ---	1-11, 15-37
X	TAKAHASHI N. ET AL.: "Periodicity of leucine and tandem repetition of a 24-amino acid segment in the primary structure of leucine-rich alpha2-glycoprotein of human serum" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA, vol. 82, April 1985, pages 1906-1910, XP002083674 see page 1908; figure 1 --- -/--	1-37

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

9 November 1998

Date of mailing of the international search report

08.02.99

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Macchia, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01222

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EMBL Emest8, Entry HS1227154 Accession number AA429129 25 May 1997 100% identity with Seq.ID:38 nt.16-64 XP002083675 see the whole document ---	3-8, 15-37
A	YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator" GENE, vol. 163, 1995, pages 193-196, XP002053953 see abstract ---	12,13
A	LIN Y. ET AL.: "Inhibition of nuclear translocation of transcription factor NF-kB by a synthetic peptide containing a cell membrane-permeable moti and nuclear localization sequence" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 24, 16 June 1995, pages 14255-14258, XP002050723 cited in the application see abstract ---	14
A	WO 96 34981 A (GENSET (FR); NICOLAEVNA MERENKOVA I.; DUMAS MILNE EDWARDS J.-B.G.) 7 November 1996 cited in the application ---	
A	KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application ---	
A	EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 cited in the application ---	
A	CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996, pages 327-336, XP002081729 cited in the application ---	
A	WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 ---	
	--- -/--	

INTERNATIONAL SEARCH REPORT

International Application No

PCT, IB 98/01222

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993, pages 600-603, XP000673204	
A	HEIJNE VON G.: "A new method for predicting signal sequence cleavage sites" NUCLEIC ACIDS RESEARCH, vol. 14, no. 11, 1986, pages 4683-4690, XP002053954 cited in the application	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 98/01222

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-37 all partially (Invention 1. on continuation-sheet)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Invention 1: Claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:292, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

2. Claims: Inventions 2-254: Claims 1-37 all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-291, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 293, invention 3 is limited to Seq.ID:40 and 294,....., invention 254 is limited to Seq.ID:291 and 545).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 98/01222

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9845437	A	15-10-1998	AU	6956798 A	30-10-1998

WO 9634981	A	07-11-1996	FR	2733765 A	08-11-1996
			FR	2733762 A	08-11-1996
			AU	5982996 A	21-11-1996
			CA	2220045 A	07-11-1996
			EP	0824598 A	25-02-1996

EP 0625572	A	23-11-1994	JP	6153953 A	03-06-1994
			WO	9408001 A	14-04-1994
			US	5597713 A	28-01-1997

WO 9707198	A	27-02-1997	US	5707829 A	13-01-1998
			AU	6712396 A	18-02-1997
			AU	6768596 A	12-03-1997
			CA	2227220 A	06-02-1997
			CA	2229208 A	27-02-1997
			EP	0839196 A	06-05-1998
			EP	0851875 A	08-07-1998
			WO	9704097 A	06-02-1997



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47		A3	(11) International Publication Number: WO 99/06548 (43) International Publication Date: 11 February 1999 (11.02.99)
(21) International Application Number: PCT/IB98/01222 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,135 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Régimbeau, 26, Avenue Kléber, F-75116 Paris (FR).			(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>With amended claims.</i> (88) Date of publication of the international search report: 8 April 1999 (08.04.99) Date of publication of the amended claims: 3 June 1999 (03.06.99)
(54) Title: 5'ESTs FOR NON TISSUE SPECIFIC SECRETED PROTEINS			
(57) Abstract The sequences of 5'ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5'ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5'ESTs. The 5'ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5'ESTs. The 5'ESTs may also be used to design expression vectors and secretion vectors.			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

AMENDED CLAIMS

[received by the International Bureau on 8 April 1999 (08.04.99);
original claims 1-37 replaced by new claims 1-37 (5 pages)]

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 38-291 or comprising a sequence complementary thereto.
2. The nucleic acid of Claim 1, wherein said nucleic acid is recombinant.
- 5 3. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-291 or one of the sequences complementary thereto, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
- 10 4. A purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-291 or one of the sequences complementary thereto, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
- 15 5. The nucleic acid of Claim 4, wherein said nucleic acid is recombinant.
6. A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-291 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-291, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated
20 entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
7. The nucleic acid of Claim 6, wherein said nucleic acid is recombinant.
8. A purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID
25 NO: 38-291, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
9. A purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-291 or having a sequence complementary thereto.
- 30 10. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 38-291 which encode a signal peptide.
11. A purified or isolated polypeptides comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-291.
12. A vector encoding a fusion protein comprising a polypeptide and a signal
35 peptide, said vector comprising a first nucleic acid encoding a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-291 operably linked to a second nucleic acid encoding a polypeptide.
13. A method of directing the extracellular secretion of a polypeptide or the insertion of a polypeptide into the membrane comprising the steps of:

obtaining a vector according to Claim 12; and

introducing said vector into a host cell such that said fusion protein is secreted into the extracellular environment of said host cell or inserted into the membrane of said host cell.

5 14. A method of importing a polypeptide into a cell comprising contacting said cell with a fusion protein comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-291 operably linked to said polypeptide.

 15. A method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-291, comprising the steps of:

10 obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-291;

 contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-291 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA;

 identifying a cDNA which hybridizes to said detectable probe; and

15 isolating said cDNA which hybridizes to said probe.

 16. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-291 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 15.

20 17. The cDNA of Claim 16 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-291.

 18. A method of making a cDNA comprising one of the sequences of SEQ ID NOs: 38-291, comprising the steps of:

25 contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

 hybridizing said first primer to said polyA tail;

 reverse transcribing said mRNA to make a first cDNA strand;

30 making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-291; and

isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

19. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-291 or a
5 fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 18.

20. The cDNA of Claim 19 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-291.

21. The method of Claim 18, wherein the second cDNA strand is made by:
10 contacting said first cDNA strand with a first pair of primers, said first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-291 and a third primer having a sequence therein which is included within the sequence of said first primer;

performing a first polymerase chain reaction with said first pair of nested primers to
15 generate a first PCR product;

contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NO:s 38-291 , and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and
20 performing a second polymerase chain reaction, thereby generating a second PCR product.

22. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-291, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of
25 Claim 21.

23. The cDNA of Claim 22 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-291.

24. The method of Claim 18 wherein the second cDNA strand is made by:
contacting said first cDNA strand with a second primer comprising at least 15
30 consecutive nucleotides of the sequences of SEQ ID NOs: 38-291;
hybridizing said second primer to said first strand cDNA; and

extending said hybridized second primer to generate said second cDNA strand.

25. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-291 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable
5 by the method of Claim 24.

26. The cDNA of Claim 25, wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-291.

27. A method of making a protein comprising one of the sequences of SEQ ID NO: 292-545, comprising the steps of:
10 obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NO: 38-291;

inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;
introducing said expression vector into a host cell whereby said host cell produces the
15 protein encoded by said cDNA; and
isolating said protein.

28. An isolated protein obtainable by the method of Claim 27.

29. A method of obtaining a promoter DNA comprising the steps of:
obtaining DNAs located upstream of the nucleic acids of SEQ ID NO: 38-291 or the
20 sequences complementary thereto;

screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and

isolating said DNA comprising said identified promoter.

30. The method of Claim 29, wherein said obtaining step comprises chromosome
25 walking from said nucleic acids of SEQ ID NO: 38-291 or sequences complementary thereto.

31. The method of Claim 30, wherein said screening step comprises inserting said upstream sequences into a promoter reporter vector.

32. The method of Claim 30, wherein said screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription
30 start sites.

33. An isolated promoter obtainable by the method of Claim 32.

34. An isolated or purified protein comprising one of the sequences of SEQ ID NO: 292-545.

35. In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one of the sequences of
5 SEQ ID NOs: 38-291, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-291, or a fragment thereof of at least 15 consecutive nucleotides.

36. The array of Claim 35 including therein at least two of the sequences of SEQ ID NOs: 38-291, the sequences complementary to the sequences of SEQ ID NOs: 38-291, or fragments thereof of at least 15 consecutive nucleotides.

10 37. The array of Claim 35 including therein at least five of the sequences of SEQ ID NOs: 38-291, the sequences complementary to the sequences of SEQ ID NOs: 38-291, or fragments thereof of at least 15 consecutive nucleotides.

